

RAW SEQUENCE LISTING

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Application Serial Number: 10/532,489
Source: PCT
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RAW SEQUENCE LISTING

DATE: 03/14/2006

PATENT APPLICATION: US/10/532,489

TIME: 10:26:42

Input Set : N:\Cr3f3\RULE60\10532489.RAW.txt

Output Set: N:\CRF4\03142006\J532489.raw

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1 <110> APPLICANT: LUDWIG INSTITUTE FOR CANCER RESEARCH
2   SCANLAN, MATTHEW
3   RITTER, GERD
4   OLD, LLOYD
5   JUNGBLUTH, ACHIM
6 <120> TITLE OF INVENTION: A34 AND A33-LIKE 3 DNA, PROTEINS, ANTIBODIES THERETO
7   AND METHODS OF TREATMENT USING SAME
8 <130> FILE REFERENCE: 029065.51088WO
9 <140> CURRENT APPLICATION NUMBER: US/10/532,489
10 <141> CURRENT FILING DATE: 2005-04-22
11 <150> PRIOR APPLICATION NUMBER: PCT/US03/33707
12 <151> PRIOR FILING DATE: 2003-10-23
13 <150> PRIOR APPLICATION NUMBER: 60/420,285
14 <151> PRIOR FILING DATE: 2002-10-23
15 <160> NUMBER OF SEQ ID NOS: 50
16 <170> SOFTWARE: PatentIn Ver. 2.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 387
20 <212> TYPE: PRT
21 <213> ORGANISM: Homo sapiens
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26             20             25             30
27   Val Thr Val Gly Ser Asn Val Thr Leu Ile Cys Ile Tyr Thr Thr Thr
28             35             40             45
29   Val Ala Ser Arg Glu Gln Leu Ser Ile Gln Trp Ser Phe Phe His Lys
30             50             55             60
31   Lys Glu Met Glu Pro Ile Ser Ile Tyr Phe Ser Gln Gly Gly Gln Ala
32             65             70             75             80
33   Val Ala Ile Gly Gln Phe Lys Asp Arg Ile Thr Gly Ser Asn Asp Pro
34             85             90             95
35   Gly Asn Ala Ser Ile Thr Ile Ser His Met Gln Pro Ala Asp Ser Gly
36             100            105            110
37   Ile Tyr Ile Cys Asp Val Asn Asn Pro Pro Asp Phe Leu Gly Gln Asn
38             115            120            125
39   Gln Gly Ile Leu Asn Val Ser Val Leu Val Lys Pro Ser Lys Pro Leu
40             130            135            140
41   Cys Ser Val Gln Gly Arg Pro Glu Thr Gly His Thr Ile Ser Leu Ser
42             145            150            155            160
43   Cys Leu Ser Ala Leu Gly Thr Pro Ser Pro Val Tyr Tyr Trp His Lys
44             165            170            175

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45      Leu Glu Gly Arg Asp Ile Val Pro Val Lys Glu Asn Phe Asn Pro Thr
46              180                      185                      190
47      Thr Gly Ile Leu Val Ile Gly Asn Leu Thr Asn Phe Glu Gln Gly Tyr
48              195                      200                      205
49      Tyr Gln Cys Thr Ala Ile Asn Arg Leu Gly Asn Ser Ser Cys Glu Ile
50              210                      215                      220
51      Asp Leu Thr Ser Ser His Pro Glu Val Gly Ile Ile Val Gly Ala Leu
52      225                      230                      235                      240
53      Ile Gly Ser Leu Val Gly Ala Ala Ile Ile Ile Ser Val Val Cys Phe
54              245                      250                      255
55      Ala Arg Asn Lys Ala Lys Ala Lys Ala Lys Glu Arg Asn Ser Lys Thr
56              260                      265                      270
57      Ile Ala Glu Leu Glu Pro Met Thr Lys Ile Asn Pro Arg Gly Glu Ser
58              275                      280                      285
59      Glu Ala Met Pro Arg Glu Asp Ala Thr Gln Leu Glu Val Thr Leu Pro
60              290                      295                      300
61      Ser Ser Ile His Glu Thr Gly Pro Asp Thr Ile Gln Glu Pro Asp Tyr
62      305                      310                      315                      320
63      Glu Pro Lys Pro Thr Gln Glu Pro Ala Pro Glu Pro Ala Pro Gly Ser
64              325                      330                      335
65      Glu Pro Met Ala Val Pro Asp Leu Asp Ile Glu Leu Glu Leu Glu Pro
66              340                      345                      350
67      Glu Thr Gln Ser Glu Leu Glu Pro Glu Pro Glu Pro Glu Pro Glu Ser
68              355                      360                      365
69      Glu Pro Gly Val Val Val Glu Pro Leu Ser Glu Asp Glu Lys Gly Val
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71      Val Lys Ala
72      385
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76 <212> TYPE: PRT
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81      Val Thr Val Asp Ala Ile Ser Val Glu Thr Pro Gln Asp Val Leu Arg
82              20           25           30
83      Ala Ser Gln Gly Lys Ser Val Thr Leu Pro Cys Thr Tyr His Thr Ser
84              35           40           45
85      Thr Ser Ser Arg Glu Gly Leu Ile Gln Trp Asp Lys Leu Leu Leu Thr
86              50           55           60
87      His Thr Glu Arg Val Val Ile Trp Pro Phe Ser Asn Lys Asn Tyr Ile
88              65           70           75           80
89      His Gly Glu Leu Tyr Lys Asn Arg Val Ser Ile Ser Asn Asn Ala Glu
90              85           90           95
91      Gln Ser Asp Ala Ser Ile Thr Ile Asp Gln Leu Thr Met Ala Asp Asn
92              100          105          110
93      Gly Thr Tyr Glu Cys Ser Val Ser Leu Met Ser Asp Leu Glu Gly Asn
94              115          120          125

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95      Thr Lys Ser Arg Val Arg Leu Leu Val Leu Val Pro Pro Ser Lys Pro
96          130                      135                      140
97      Glu Cys Gly Ile Glu Gly Glu Thr Ile Ile Gly Asn Asn Ile Gln Leu
98          145                      150                      155                      160
99      Thr Cys Gln Ser Lys Glu Gly Ser Pro Thr Pro Gln Tyr Ser Trp Lys
100          165                      170                      175
101      Arg Tyr Asn Ile Leu Asn Gln Glu Gln Pro Leu Ala Gln Pro Ala Ser
102          180                      185                      190
103      Gly Gln Pro Val Ser Leu Lys Asn Ile Ser Thr Asp Thr Ser Gly Tyr
104          195                      200                      205
105      Tyr Ile Cys Thr Ser Ser Asn Glu Glu Gly Thr Gln Phe Cys Asn Ile
106          210                      215                      220
107      Thr Val Ala Val Arg Ser Pro Ser Met Asn Val Ala Leu Tyr Val Gly
108          225                      230                      235                      240
109      Ile Ala Val Gly Val Val Ala Ala Leu Ile Ile Ile Gly Ile Ile Ile
110          245                      250                      255
111      Tyr Cys Cys Cys Cys Arg Gly Lys Asp Asp Asn Thr Glu Asp Lys Glu
112          260                      265                      270
113      Asp Ala Arg Pro Asn Arg Glu Ala Tyr Glu Glu Pro Pro Glu Gln Leu
114          275                      280                      285
115      Arg Glu Leu Ser Arg Glu Arg Glu Glu Glu Asp Asp Tyr Arg Gln Glu
116          290                      295                      300
117      Glu Gln Arg Ser Thr Gly Arg Glu Ser Pro Asp His Leu Asp Gln
118          305                      310                      315
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122 <212> TYPE: DNA
123 <213> ORGANISM: Homo sapiens
124 <400> SEQUENCE: 3
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126      aatttgtaaa aaataccctc gaagattcag gaatgaagct tctgtgtgaa ggattaaaac 120
127      agcccaactg tgtattacag acattgaggt ggtaccgggtg ccttatctct tctgcttctt 180
128      gtggggctct agcagctgtt cttagcacca gtcagtggct cactgaactg gaatttagtg 240
129      agacaaaact ggaagcttca gctttgaaat tgctctatgg aggcttaaaa gatccaaatt 300
130      gcaaattaca gaagctcaac ttgcagtttt ctttatctgt aaccgctgca aaacttccag 360
131      ttggaatggt tggaattgt tctggtttct cgggatcatt ggtgcaatct cattttggct 420
132      actgtcagga cagttctttc aaatgtgatc tttgtaagct gctctggcct tccaccagag 480
133      ttgctgctgc aaaggattgt gggagtccta agtccttcct atcagaaggg ctgaactggg 540
134      caggaagact tgaggcagtg gaggaggttt tggggtttggg ggtgcttgta cagcccggtg 600
135      acccagcatc tcagggtggg gggcattgtg aaaactatgg gtcttttaga gacttggtgg 660
136      acttagaagt caaggcagaa ccaagcctga gaaaagggtg tatggatctc cagagacca 720
137      ccctacaagt tgcctcctt tgcaaaatct tctccctcaa actatttctc tttattgcat 780
138      tgctaattc tcctggtcag gttagtgtgg tgcaagtgc catcccagac ggtttcgtga 840
139      acgtgactgt tggatcta atgtcactcta tctgcatcta caccaccact gtggcctccc 900
140      gagaacagct ttccatccag tggcttttct tccataagaa ggagatggag ccaatttcta 960
141      tttacttttc tcaagggtgga caagctgtag ccatcgggca atttaaagat cgaattacag 1020
142      ggtccaacga tccaggtaat gcatttatca ctatctcgca tatgcagcca gcagacagt 1080
143      gaatttacat ctgcgatgtt aacaaccccc cagactttct cggccaaaac caaggcatcc 1140
144      tcaacgtcag tgtgttagtg aaaccttcta agccctttg tagcgttcaa ggaagaccag 1200

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145 aaactggcca cactatttcc ctttcctgtc tctctgcgct tggaacacct tcccctgtgt 1260
146 actactggca taaacttgag ggaagagaca tcgtgccagt gaaagaaaac ttcaacccaa 1320
147 ccaccgggat tttggtcatt ggaaatctga caaatTTtga acaagggttat taccagtgtgta 1380
148 ctgccatcaa cagacttggc aatagttcct gcgaaatcga tctcacttct tcacatccag 1440
149 aagttggaat cattgttggg gccttgattg gtagcctggg aggtgccgcc atcatcatct 1500
150 ctgttggtgtg cttcgcaagg aataaggcaa aagcaaaggc aaaagaaaaga aattctaaga 1560
151 ccatcgcgga acttgagcca atgacaaaaga taaacccaag gggagaaaagc gaagcaatgc 1620
152 caagagaaga cgctacccaa ctagaagtaa ctctaccatc ttccattcat gagactggcc 1680
153 ctgataccat ccaagaacca gactatgagc caaagcctac tcaggagcct gccccagagc 1740
154 ctgccccagg atcagagcct atggcagtgc ctgaccttga catcgagctg gagctggagc 1800
155 cagaaacgca gtcggaattg gagccagagc cagagccaga gccagagtca gagcctgggg 1860
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159 <211> LENGTH: 402
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161 <213> ORGANISM: Homo sapiens
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165 Phe Ser Leu Lys Leu Phe Leu Phe Ile Ala Leu Pro Asn Ser Pro Gly
166 20 25 30
167 Gln Val Ser Val Val Gln Val Thr Ile Pro Asp Gly Phe Val Asn Val
168 35 40 45
169 Thr Val Gly Ser Asn Val Thr Leu Ile Cys Ile Tyr Thr Thr Thr Val
170 50 55 60
171 Ala Ser Arg Glu Gln Leu Ser Ile Gln Trp Ser Phe Phe His Lys Lys
172 65 70 75 80
173 Glu Met Glu Pro Ile Ser Ile Tyr Phe Ser Gln Gly Gly Gln Ala Val
174 85 90 95
175 Ala Ile Gly Gln Phe Lys Asp Arg Ile Thr Gly Ser Asn Asp Pro Gly
176 100 105 110
177 Asn Ala Ser Ile Thr Ile Ser His Met Gln Pro Ala Asp Ser Gly Ile
178 115 120 125
179 Tyr Ile Cys Asp Val Asn Asn Pro Pro Asp Phe Leu Gly Gln Asn Gln
180 130 135 140
181 Gly Ile Leu Asn Val Ser Val Leu Val Lys Pro Ser Lys Pro Leu Cys
182 145 150 155 160
183 Ser Val Gln Gly Arg Pro Glu Thr Gly His Thr Ile Ser Leu Ser Cys
184 165 170 175
185 Leu Ser Ala Leu Gly Thr Pro Ser Pro Val Tyr Tyr Trp His Lys Leu
186 180 185 190
187 Glu Gly Arg Asp Ile Val Pro Val Lys Glu Asn Phe Asn Pro Thr Thr
188 195 200 205
189 Gly Ile Leu Val Ile Gly Asn Leu Thr Asn Phe Glu Gln Gly Tyr Tyr
190 210 215 220
191 Gln Cys Thr Ala Ile Asn Arg Leu Gly Asn Ser Ser Cys Glu Ile Asp
192 225 230 235 240
193 Leu Thr Ser Ser His Pro Glu Val Gly Ile Ile Val Gly Ala Leu Ile
194 245 250 255

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195 Gly Ser Leu Val Gly Ala Ala Ile Ile Ile Ser Val Val Cys Phe Ala
196           260           265           270
197 Arg Asn Lys Ala Lys Ala Lys Ala Lys Glu Arg Asn Ser Lys Thr Ile
198           275           280           285
199 Ala Glu Leu Glu Pro Met Thr Lys Ile Asn Pro Arg Gly Glu Ser Glu
200           290           295           300
201 Ala Met Pro Arg Glu Asp Ala Thr Gln Leu Glu Val Thr Leu Pro Ser
202           305           310           315           320
203 Ser Ile His Glu Thr Gly Pro Asp Thr Ile Gln Glu Pro Asp Tyr Glu
204           325           330           335
205 Pro Lys Pro Thr Gln Glu Pro Ala Pro Glu Pro Ala Pro Gly Ser Glu
206           340           345           350
207 Pro Met Ala Val Pro Asp Leu Asp Ile Glu Leu Glu Leu Glu Pro Glu
208           355           360           365
209 Thr Gln Ser Glu Leu Glu Pro Glu Pro Glu Pro Glu Pro Glu Ser Glu
210           370           375           380
211 Pro Gly Val Val Val Glu Pro Leu Ser Glu Asp Glu Lys Gly Val Val
212           385           390           395           400
213 Lys Ala
215 <210> SEQ ID NO: 5
216 <211> LENGTH: 1045
217 <212> TYPE: DNA
218 <213> ORGANISM: Homo sapiens
219 <400> SEQUENCE: 5
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221 cagctttcca tccagtgggc tttcttccat aagaaggaga tggagccaat ttctatttac 120
222 ttttctcaag gtggacaagc tgtagccatc gggcaattta aagatcgaat tacaggggtcc 180
223 aacgatccag gtaatgcac tctactatc tcgcatatgc agccagcaga cagtgggaatt 240
224 tacatctgcg atgttaacaa cccccagac tttctcggcc aaaaccaagg catcctcaac 300
225 gtcagtgtgt tagtgaaacc ttctaagccc ctttgtagcg ttcaaggaag accagaaact 360
226 ggccacacta tttccctttc ctgtctctct gcgcttgga caccttcccc tgtgtactac 420
227 tggcataaac ttgagggaag agacatcggt ccagtgaag aaaacttcaa cccaaccacc 480
228 gggatttttg tcattggaaa tctgacaaat tttgaacaag gttattacca gtgtactgcc 540
229 atcaacagac ttggcaatag ttcctgcgaa atcgatctca cttcttcaca tccagaagtt 600
230 ggaatcattg ttggggcctt gattggtagc ctggttaggt cgcgccatcat catctctgtt 660
231 gtgtgcttcg caaggaataa ggcaaaagca aaggcaaaag aaagaaattc taagaccatc 720
232 gcggaacttg agccaatgac aaagataaac ccaaggggag aaagcgaagc aatgccaaga 780
233 gaagacgcta cccaactaga agtaactcta ccatcttcca ttcattgagac tggccctgat 840
234 accatccaag aaccagacta tgagccaaag cctactcagg agcctgcccc agagcctgcc 900
235 ccaggatcag agcctatggc agtgcccgac cttgacatcg agctggagct ggagccagaa 960
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239 <210> SEQ ID NO: 6
240 <211> LENGTH: 348
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242 <213> ORGANISM: Homo sapiens
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VERIFICATION SUMMARY

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